

## Origin and spread of a possibly invasive cryptogenic *Dictyota* species within the Mediterranean

Steen Frédérique and Olivier De Clerck

Phycology Research Group, Biology Department, Ghent University, Krijgslaan 281,  
B-9000 Ghent, Belgium  
E-mail: frederique.steen@ugent.be

The Mediterranean is a melting pot of exotic seaweed species, introduced by different vectors. The most notorious exotic alga is *Caulerpa taxifolia*, nicknamed the “killer alga”. We would like to add another exotic and possibly invasive *Dictyota* species to the growing list.

The species was first described as a recent introduction to the western Mediterranean in 2007 and from the Macaronesian islands in 2009. Unlike other *Dictyota* spp., this species is quite easily discernible by a blue iridescent rim at the edge of the thallus. From then on, new records of the species were reported steadily within the Mediterranean and even in the North-east Atlantic, indicating that the species was more widespread than originally believed. In contrary to the hypothesis of a recent introduction, molecular identification of herbarium specimen revealed the presence of the species within the Adriatic Sea as early as 1935. Until now no additional ancient herbarium records were found elsewhere. This finding raises the question whether this represents a lag phase in its spread or if the species remained unrecognized for this period of time despite the fact that the genus *Dictyota* has traditionally been well studied within the Atlanto-Mediterranean.

A global *Dictyota* phylogenetic dataset suggested Australia could be the native range of this species. Two mitochondrial markers were sequenced, both for Australian and European samples, and network analyses showed that the Australian samples indeed harbour most of the diversity, while the European samples seem more genetically depauperate. This confirmed that a Pacific origin was most likely. However, there was no reason to assume a single introduction event.

In this respect a microsatellite data set will be developed from a genomic dataset, to assess genetic divergence from Australian and European samples and if possible the directionality of the spread and the timing of introduction within the Mediterranean. We are aiming to amplify loci by multiplex PCR, and obtain sequence data in a high throughput fashion, employing an approach deviated from the principles of RADseq. This would substantially decrease the cost of microsatellite analysis, allowing us to track the invasion history of this *Dictyota* sp.